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Establishing of maternal lineages in Hungarian native Tsigai sheep breed*

Annus, K.[1] *- J. Oláh*[2] *- M. Prikoszovich*[3] *-*
Á. Maróti-Agóts[1] *- A. Gáspárdy*[1]

[1]Szent István University, Faculty of Veterinary Science, Budapest, Hungary
[2]Debrecen University, Faculty of Agricultural and Food Sciences and Environmental Management, Debrecen, Hungary
[3]Eötvös Loránd University, Faculty of Science, Budapest, Hungary

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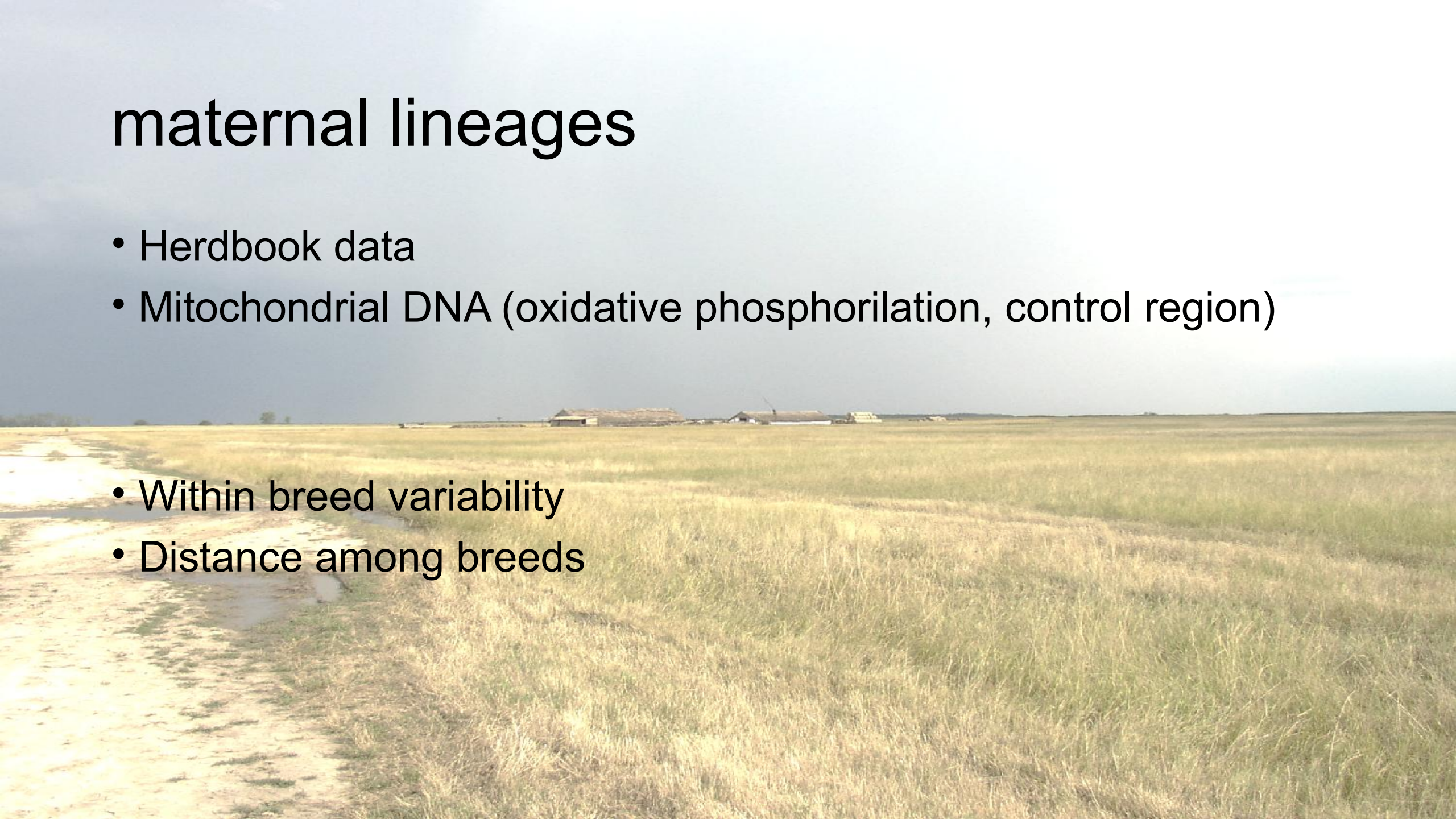
Summary

- The Tsigai got into Hungary around 1700. The claim of the blaze factories inspired the farmers in Transylvania to change the rough woolly Curkan to Tsigai, which produced more soft wool. The traditionally multipurpose Tsigai breed is registered within the sheep group of mountain origin. In the course of its spreading in the Carpathian-basin the breed has been adapted to the different geographical and climatic conditions very well.
- Nowadays, the Tsigai population in Hungary can be divided into two main groups of animals by the purpose: the gene reserve variant and the single-purpose milking variant, latest registered as a new breed officially. The mountain type is the smallest; it reaches 30-40 kg by first year of age. The lowland ecotype grows larger on the rich meadows of the Hungarian Great Plain: with 45-55 kg yearling weight. The third type is the high yielders of milk, which became a quite heavy breed, the milking Tsigai by the present. According to the Hungarian Association of Sheep and Goat Breeders of Tsigai sheep the number of female individuals is constant in our days. The age at first lambing is nearly 2 years which is advantageous thus the late sexual maturity of the breed is not endangered.
- We got the pedigree data from the Hungarian Association of Sheep and Goat Breeders. The animals were registered in the re-established herd-book from 1995. The database contains 28,284 individuals with all of their data. After analysing the data according to the maternal lineages, the 56 „most ancient” families with the longest pedigree were selected for. The families chosen contain at least seven generations. The distinction of the families is very crucial in the maintenance of the genetic diversity. Representatives of the ancient families are basically farm-specific.
- We took blood sample from the living members of these families, from 2 individuals of each. For the further examination we would like to use the mitochondrial DNA. The mitochondria provide a possible mechanism of cytoplasmic inheritance, being inherited exclusively through the maternal lineage and containing a closed loop of DNA coding for genes, for proteins of the electron transport chain, essential for producing ATP from ADP. Each cell contains many copies of mtDNA which, except in very rare cases of heteroplasmy, are identical and shared by all members of the maternal lineage.
- From our investigation we hope the further maintenance of the genetic variability which adapts well to different protected living environment.

maternal lineages

- Herdbook data
- Mitochondrial DNA (oxidative phosphorilation, control region)

- Within breed variability
- Distance among breeds



Genetic variability

- Selection (mutation)
- Generation interval
- Relationship
- Sex ratio

Outbred populations

Maximalisation of **Effective population size (Ne)**:

$$\mathbf{Ne} = 4 * (♂ * ♀)/(♂ + ♀)$$

♂ = no. of males, ♀ = no. of females

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1. Example (sex ratio 1:1):

♂ = 20, ♀ = 20

$Ne_1 = 4*(20*20)/(20+20)$

$Ne_1 = 4*(400)/(40)$

$Ne_1 = 40$

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2. Example (sex ratio 1:20):

♂ = 1, ♀ = 20

$Ne_2 = 4*(1*20)/(1+20)$

$Ne_2 = 4*(20)/(21)$

$Ne_2 = 3{,}8$

Abb. 25. Stutenherde in Lipizza, Gemälde von George Hamilton 1727 (Foto Habe).

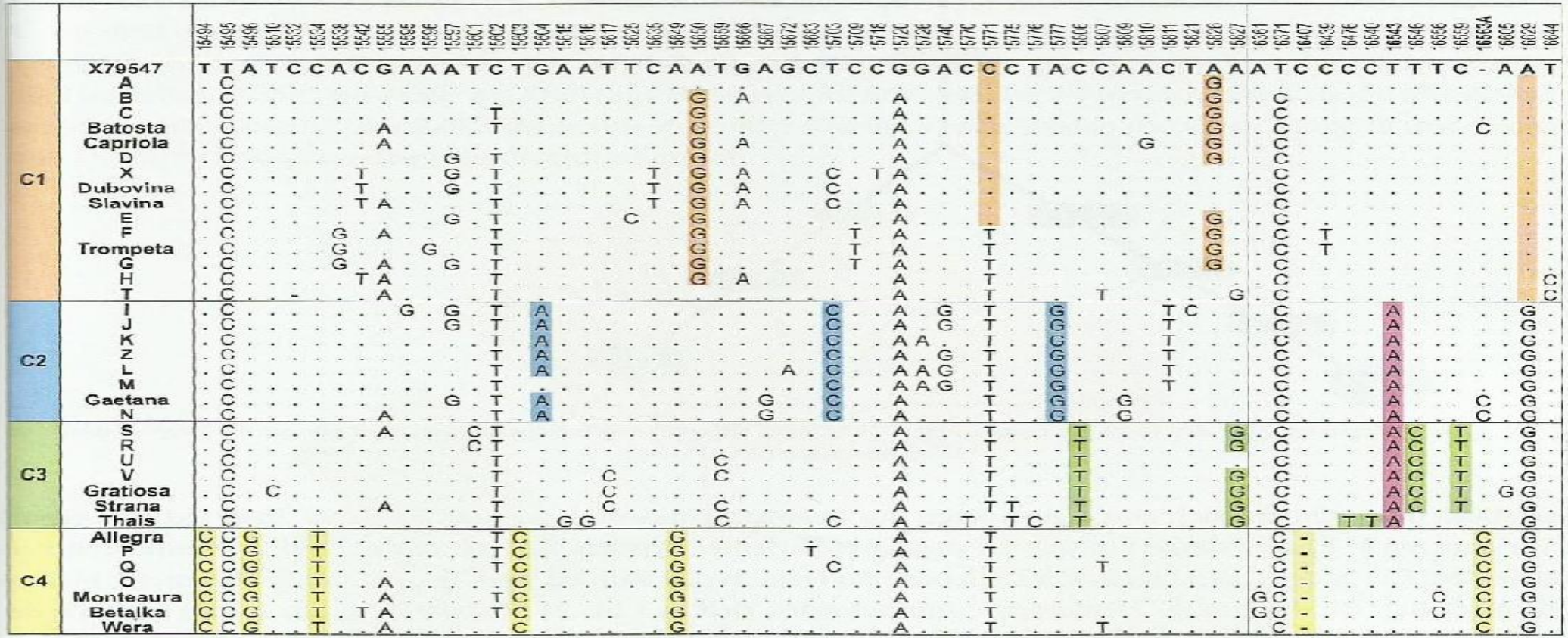


Abb. 2. Zusammenfassung der Lipizzaner mtDNA Polymorphismen und Gruppierung der Lipizzaner Haplotypen in vier Haplotypen-Hauptgruppen (Grafik Dové).

Gestüt	Batosta	Capriola	Slavina	Betalka	Allegra	Dubovina	Gactana	Gratiosa	Monteaura	Wera	P	M	G	B	J	U	X	O	I	Q	R	V	Strana	Thais	Trompeta	L	H	D	E	A	K	S	T	Z	C	F	N
Piber	4	18	2	11	3	6	3	1		3	1	1	2	2	2	9		3	1																		
Monterotondo	4	7	5	1	7	5		1	2					2	5	2	5																				
Dakovo	3		5		1	3	5		2																	2	3	2	13								
Lipica	4	9	5	4	5	2	2	2	2	3													2	2	2												
Szilvasvarad	12	20			7		1					5							19	6	2	1															
Beclean	1	5									4		3																1	4	1	1					
Fagaras	3	34									3	8	15																3	5	1	1	1	1	4	5
Topolčianky	11	17	1				3			6																											
Total	42	110	18	16	23	16	14	4	6	12	8	14	20	4	7	11	5	3	20	6	2	1	2	2	2	2	3	2	13	4	9	2	2	1	1	4	5
Frequenz (%)	10,1	26,4	4,3	3,8	5,5	3,8	3,4	0,7	1,4	2,9	1,9	3,4	4,8	1	1,7	2,6	1,2	0,7	4,8	1,4	0,5	0,2	0,5	0,5	0,5	0,5	0,7	0,5	3,1	1	2,2	0,5	0,5	0,2	0,2	1	1,2

Abb. 7. Verteilung der mtDNA Haplotypen in acht Lipizzaner Gestüten. Die Frequenzen der einzelnen Haplotypen sind in der unteren Zeile als Prozentanteil von allen analysierten Tieren angegeben (Grafik Dové).

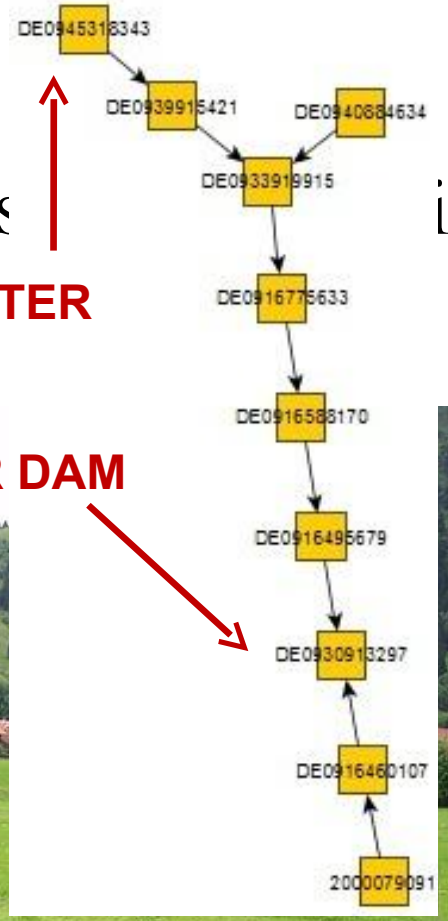
“Verband schweizerischer Braunviehzucht-Genossenschaften” 1897

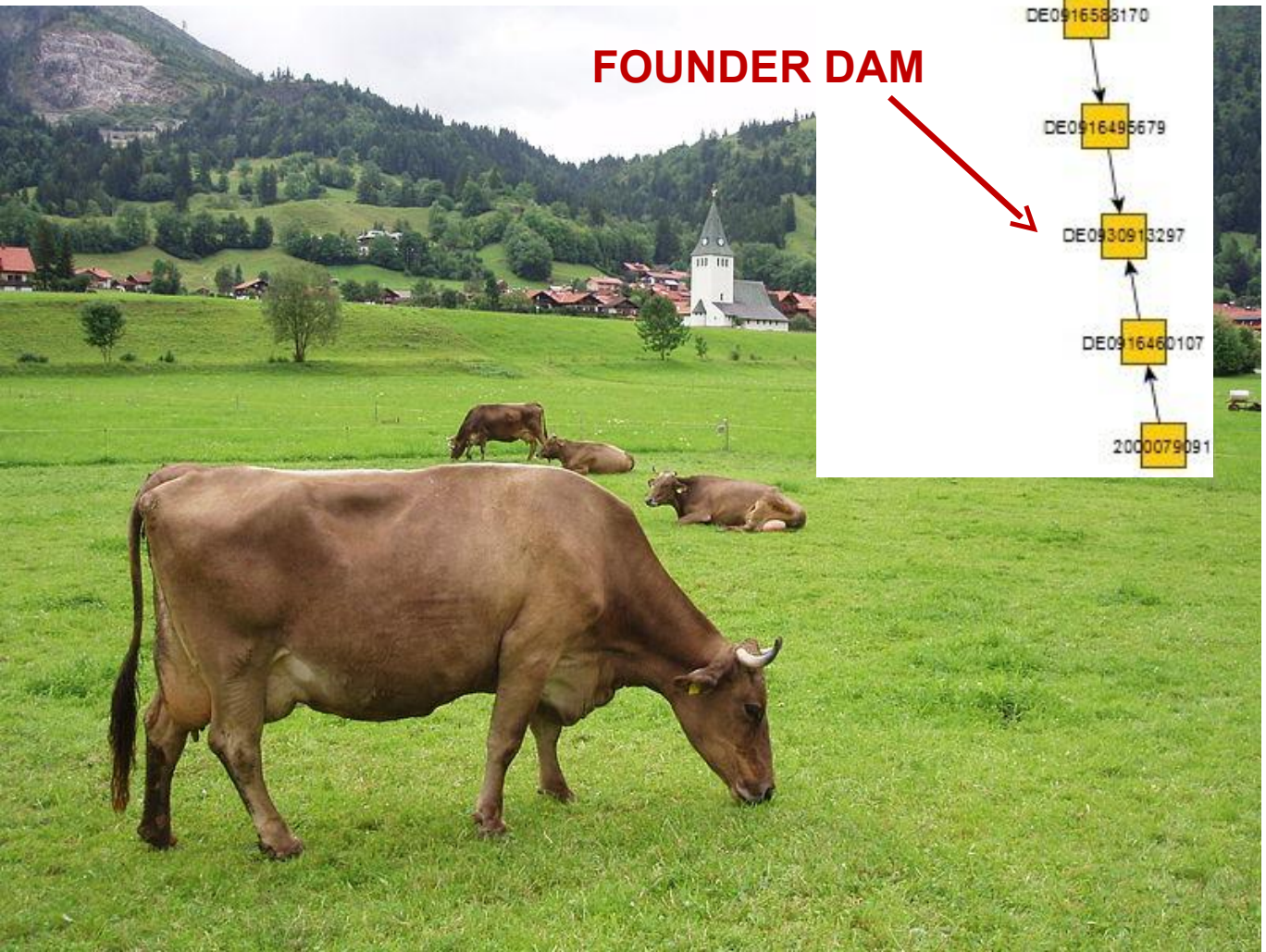
- 60 Algäuer cows (≈100)
- 48 families (13 CH, 35 DE)
- 1.25 (1-3) representatives/family
- 5.7 generations (2-7)

“Verband schweizeris iehzucht-Genossenschaften” 1897

LIVING DAUGHTER

FOUNDER DAM





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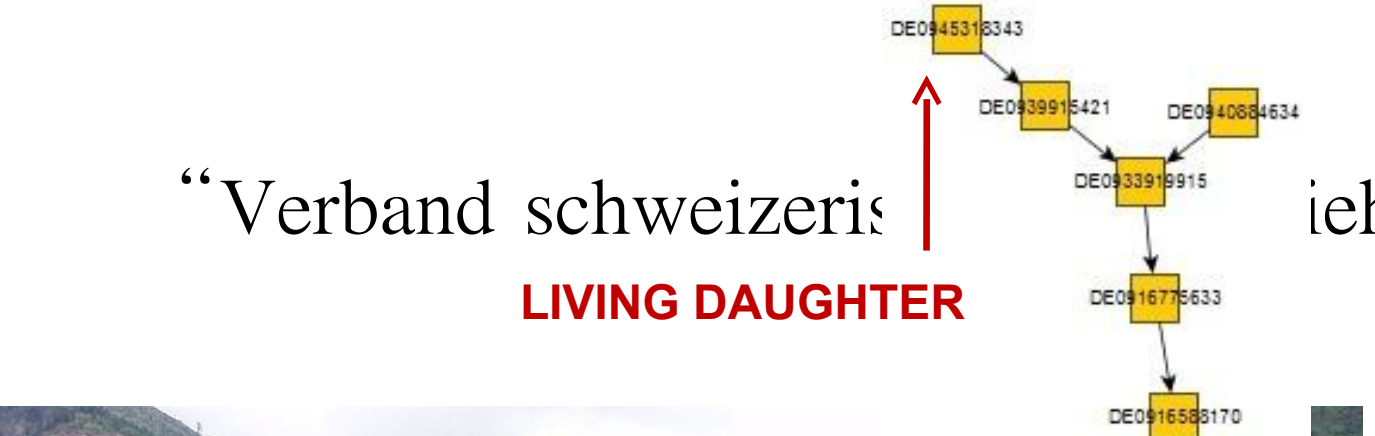
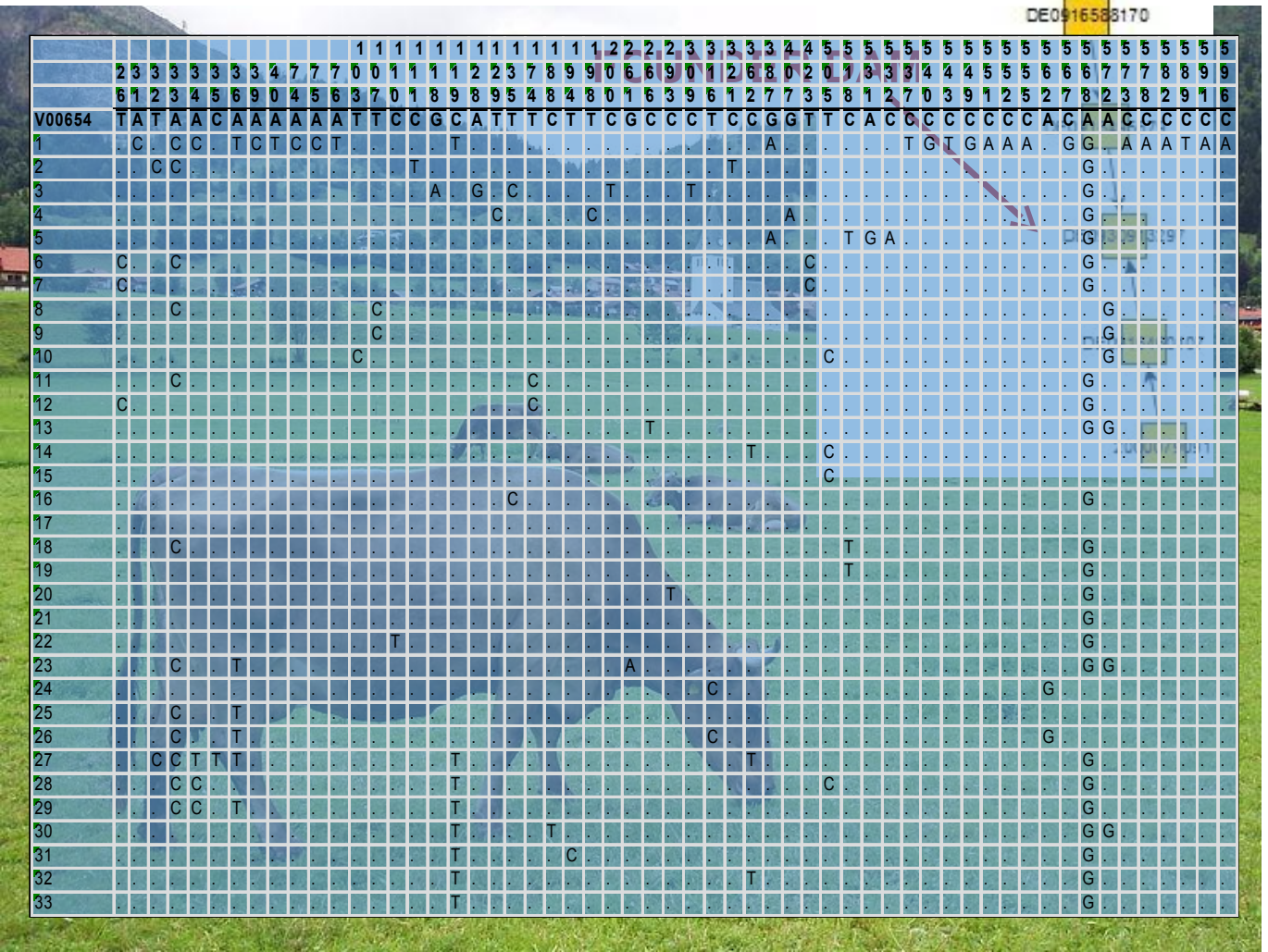


LIVING DAUGHTER



- 60 Algäuer cows (≈100)
- 48 families (13 CH, 35 DE)
- 1.25 (1-3) representatives/family
- 5.7 generations (2-7)
- 57 polymorphic sites (611 bp)
- 33 haplotypes

Hungarian native tsigai

Great Plain lowland ecotype

Carpathian mountain ecotype

Southland milking type

Pedigree analysis

Generation interval

	mean	median
parent - offspring	4.28	3.99
dam - offspring	4.46	4.02
sire - offspring	4.10	3.93
dam - daughter	4.39	4.01
dam - son	4.53	4.04
sire - daughter	4.13	3.93
sire - son	4.06	3.92

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Pedigree analysis

Inbreeding coefficient (NS=non significant difference)

	all animals (n=28400)	breeding animals (n=4574)
inbred individuals	7902	1170
proportion of inbred individuals (%)	27.94	11.9
inbreeding coefficient total population	0.01491 (0.00 - 0.44189)	0.016295^{NS} (0.00 - 0.397220)
inbreeding coefficient inbred share population	0.05688 (0.00024 - 0.44189)	0.059235^{NS} (0.000490 - 0.397220)

Pedigree analysis

- total number of families: 3316 (23932 individuals)
- number of families with actually living descendants: 1469
- „ancient” families
- 56 maternal lineages

generation	number of families
9	3
8	19
7	34

Pedigree analysis

- total number of families: 3316 (23932 individuals)
- number of families with actually living descendants: 1469
- „ancient” families
- 56 maternal lineages (sample for mtDNA analysis)

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9	3
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Authors like to thank to the MJKSZ, farmers and particularly to the fellowship „Research Faculty” (8525-5/2014/TUDPOL; 15269 Population genetic evaluation of native breeds for grounding of an up-to-date preservation) supported by Ministry of Human Capacity for 2014.